

38	52.8	10.1	129149	46	HS510D11	Z98044 Human DNA s
c 39	52.8	10.1	137143	55	AC068496	AC068496 Mus muscu
c 40	52.6	10.0	175280	49	AC023327	AC023327 Homo sapi
c 41	52.6	10.0	177568	46	HS388M5	Z97055 Human DNA s
c 42	52.6	10.0	206051	50	AC024914	AC024914 Mus muscu
c 43	52.2	10.0	153147	46	HS13D10	AL021407 Homo sapi
44	52.2	10.0	155344	64	AL161899	AL161899 Homo sapi
c 45	52.2	10.0	170356	88	AF259072	AF259072 Mus muscu

# ALIGNMENTS

## RESULT 1

CVU20341  
 LOCUS CVU20341 8158 bp DNA circular VRL 25-OCT-1995  
 DEFINITION Cassava vein mosaic virus, complete genome.  
 ACCESSION U20341  
 VERSION U20341.1 GI:665931  
 KEYWORDS  
 SOURCE Cassava vein mosaic virus.  
 ORGANISM Cassava vein mosaic virus  
 Viruses; Retroid viruses.  
 REFERENCE 1 (bases 1 to 8158)  
 AUTHORS Calvert, L.A., Ospina, M.D. and Shepherd, R.J.  
 TITLE Characterization of cassava vein mosaic virus: a distinct plant  
 pararetrovirus  
 JOURNAL J. Gen. Virol. 76 (Pt 5), 1271-1278 (1995)  
 MEDLINE 95248298  
 REFERENCE 2 (bases 1 to 8158)  
 AUTHORS Calvert, L.A.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-JAN-1995) Lee A. Calvert, Virology Unit, Centro  
 Internacional de Agricultura Tropical, A.A. 6713, Cali, Valle,  
 Colombia

FEATURES Location/Qualifiers  
 source 1..8158  
 /organism="Cassava vein mosaic virus"  
 /specific\_host="Manihot esculenta"  
 /db\_xref="taxon:38062"  
 /clone="pCVMV141"  
 CDS 30..4148  
 /note="ORF 1"  
 /codon\_start=1  
 /protein\_id="AAA79871.1"  
 /db\_xref="GI:665932"  
 /translation="MDSKDFQTQLNLEHSYKVNTPQLKLPIDSYIQYGGFTYANFTPTYYI  
 HGGDGFGEHKQLNWTNKLWNKLGKLNKDTQILMQNNISEEQHNELISLEAQKIARE  
 NLADRINYLQNINTSIDFKLWKNKENLERQELLRLQINELKEEIKSLKNIPSTVAII  
 PTNTYITIMIRTETEDWKYFKYIEKELVQNKTEAIAKILDNSYIINDNLGLLYERYEE  
 INTPPKPYKRETI FDT PQYAKYIRNQKRQEYEQQLKKNENKEYQEFLENKEQ  
 QKDKGKGTQVYPTLII PDIKPEKQKKEDMMLEMIKNLQNELEQLKIQRHKEHEKQAE  
 LTKIQMLEEEEELEELDPNLEKEVLNNIQNIQISSDISESESEINEISDNETEIQISGSD  
 SDYNNENQINVKIEGEEYKDNRYRYKPPPYKDDIRRERQYKQSSQGRADYIKNRR  
 EEFESTYQANMNTTINDSGEILNLDCTTPEEAEDRIKQWTSMSIALVKQLSNEQAK  
 QFIRRTFFIGNVKEWYKNLTNEAKQKLEGNAPLLSLTHMELGLRAEFGKLGIESDVEKH  
 EKKTSIARHKILQLQICSMHDQNLAFLCEFEYYSANYTEASESINLMFYSKLP

85: gb\_htg21:\*  
 86: gb\_htg22:\*  
 87: gb\_htg23:\*  
 88: gb\_ro:\*  
 89: gb\_sts1:\*  
 90: gb\_sts2:\*  
 91: gb\_sy:\*  
 92: gb\_un:\*  
 93: gb\_vil:\*  
 94: gb\_vi2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	ID	
	1	514.6	98.2	8158	93 CVU20341	U20341 Cassava vei
	2	514.6	98.2	8159	93 CVU59751	U59751 Cassava vei
c	3	77	14.7	7218	5 I66494	I66494 Sequence 14
	4	60.4	11.5	112585	46 HS1059E7	AL023095 Human DNA
	5	59	11.3	276598	37 AC012382	AC012382 Mus muscu
	6	58.4	11.1	193432	57 AC073290	AC073290 Mus muscu
	7	58.2	11.1	259421	57 AC073689	AC073689 Mus muscu
c	8	58	11.1	171743	53 AC055806	AC055806 Homo sapi
	9	57.6	11.0	204985	57 AC073938	AC073938 Mus muscu
c	10	57.6	11.0	237908	47 AC020971	AC020971 Mus muscu
	11	57	10.9	163229	10 AC009039	AC009039 Homo sapi
	12	56.8	10.8	211308	57 AC073613	AC073613 Homo sapi
	13	56.2	10.7	513	88 RNU83985	U83985 Rattus norv
	14	56.2	10.7	60058	48 AC022549	AC022549 Mus muscu
	15	56.2	10.7	147266	10 AC005913	AC005913 Homo sapi
	16	56.2	10.7	159818	27 AC007337	AC007337 Homo sapi
	17	56.2	10.7	204318	88 AC026387	AC026387 Mus muscu
c	18	55.6	10.6	115976	57 AC073502	AC073502 Homo sapi
c	19	55.6	10.6	153664	53 AC040971	AC040971 Homo sapi
c	20	55.2	10.5	136037	9 AC004104	AC004104 Homo sapi
c	21	55	10.5	161996	63 AL133401	AL133401 Mus muscu
	22	55	10.5	181636	50 AC025108	AC025108 Homo sapi
	23	55	10.5	194615	36 AC010184	AC010184 Homo sapi
c	24	55	10.5	200275	57 AC073883	AC073883 Mus muscu
	25	54.6	10.4	71618	7 AB012240	AB012240 Arabidops
	26	54.6	10.4	200573	49 AC024116	AC024116 Mus muscu
c	27	54.4	10.4	212042	57 AC073904	AC073904 Homo sapi
	28	54.2	10.3	147156	56 AC068998	AC068998 Mus muscu
c	29	54	10.3	35875	35 AP000454	AP000454 Homo sapi
c	30	54	10.3	91748	88 AF177767	AF177767 Mus muscu
c	31	54	10.3	169328	35 AP000472	AP000472 Homo sapi
	32	54	10.3	183330	38 AC015932	AC015932 Mus muscu
c	33	54	10.3	340000	35 AP001683	AP001683 Homo sapi
	34	53.4	10.2	131169	84 AL356779	AL356779 Homo sapi
c	35	53.4	10.2	165313	84 AL356742	AL356742 Homo sapi
	36	53	10.1	53889	8 F14010	AC026234 Sequence
	37	53	10.1	221285	49 AC023611	AC023611 Mus muscu

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 17, 2000, 01:31:17 ; Search time 990.18 Seconds  
(without alignments)  
2311.309 Million cell updates/sec

Title: US-09-202-838-3  
Perfect score: 524  
Sequence: 1 ggtaccagaaggtaattatc.....aaatttgtaagtttgaattc 524

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues

Total number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_bal:\*  
2: gb\_ba2:\*  
3: gb\_om:\*  
4: gb\_ov:\*  
5: gb\_pat:\*  
6: gb\_ph:\*  
7: gb\_pl1:\*  
8: gb\_pl2:\*  
9: gb\_pr1:\*  
10: gb\_pr2:\*  
11: gb\_pr3:\*  
12: em\_fun:\*  
13: em\_hum1:\*  
14: em\_hum2:\*  
15: em\_in:\*  
16: em\_om:\*  
17: em\_or:\*  
18: em\_ov:\*  
19: em\_pat:\*  
20: em\_ph:\*  
21: em\_pl:\*  
22: em\_ro:\*  
23: em\_sts:\*  
24: em\_sy:\*  
25: em\_un:\*  
26: em\_vi:\*  
27: gb\_htg1:\*

28: gb\_htg2:\*  
29: gb\_in1:\*  
30: gb\_in2:\*  
31: em\_ba1:\*  
32: em\_ba2:\*  
33: em\_hum3:\*  
34: em\_hum4:\*  
35: gb\_pr4:\*  
36: gb\_htg3:\*  
37: gb\_htg4:\*  
38: gb\_htg5:\*  
39: gb\_htg6:\*  
40: gb\_htg7:\*  
41: em\_htg1:\*  
42: em\_htg2:\*  
43: em\_htg3:\*  
44: em\_hum5:\*  
45: gb\_pl3:\*  
46: gb\_pr5:\*  
47: gb\_htg8:\*  
48: gb\_htg9:\*  
49: gb\_htg10:\*  
50: gb\_htg11:\*  
51: gb\_htg12:\*  
52: gb\_htg13:\*  
53: gb\_htg14:\*  
54: gb\_in3:\*  
55: gb\_htg15:\*  
56: gb\_htg16:\*  
57: gb\_htg17:\*  
58: em\_htg4:\*  
59: em\_htg5:\*  
60: em\_htg6:\*  
61: em\_htg7:\*  
62: em\_hum6:\*  
63: gb\_htg18:\*  
64: gb\_htg19:\*  
65: gb\_ba3:\*  
66: em\_htg8:\*  
67: em\_htg9:\*  
68: em\_htg10:\*  
69: em\_htg11:\*  
70: em\_htg12:\*  
71: em\_htg13:\*  
72: em\_htg14:\*  
73: em\_htg15:\*  
74: em\_htg16:\*  
75: em\_htg17:\*  
76: em\_htg18:\*  
77: em\_htg19:\*  
78: em\_htg20:\*  
79: em\_htg21:\*  
80: em\_htg22:\*  
81: em\_htg23:\*  
82: gb\_pr6:\*  
83: gb\_pr7:\*  
84: gb\_htg20:\*